

## **Integrative Cancer Research Special Interest Group Teleconference**

### **Translational SIG Meeting Minutes**

Date, Time & Location:	August 2, 2004 1:00 – 2:00 EDT		
Attendees:	Edith Zang – The Institute for Cancer Prevention Naveen Vinukonda - The Institute for Cancer Prevention Michael Ochs – Fox Chase Tom Moloshok – Fox Chase Judith Goldberg – New York Tom Casavant – Holden Terry Braun - Holden Mark Watson – Wash U Steve Eschrich– Moffitt Yajun Yi – Vanderbilt Harold Reithman - Penn Claire Zhu – BAH Harshawardhan Bal - BAH Juli Klemm - BAH		
Application Presentation:	Trapss  Terry Braun (U lowa Holden) gave a presentation of Trapss. The slides can be downloaded from <a href="http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/translational">http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/translational</a> Trapss Q & A		
	<ul> <li>-How is the gene ranking determined? One way of automating this would be by running text mining routines (written in Perl, for example) on PubMed abstracts (of whole articles) and extracting genes labeled using HUGO conventions that are mentioned in the context of a particular disease or are mentioned in the context of genes that are previously known to be associated with a disease and that are described within the same sentence in the abstract or article (Harshawardhan Bal).</li> <li>- This information is entered manually into the database. We are hoping to develop automatic ranking system in the future and have some students working on this</li> </ul>		
	<ul> <li>How are genes mapped? What resources are used for annotation? It may be useful for the user to obtain quick information/annotation on a gene if links to standard NCBI resources such as LocusLink (or Entrez Gene as it will be called in the near future), UniGene or OMIM. (Harshawardhan Bal)</li> <li>Genes are anchored on the Refseq. We rely heavily on Ensembl for gene data.</li> </ul>		
	Do you use a local copy of Ensembl? This will make data access independent of the availability of the Ensembl servers and the volume of traffic accessing them; the only extra work that this would necessitate was the periodic updates of the local version (Harshawardhan Bal)  - No - this could improve the performance of the system, though speed hasn't yet been an issue. The downside is the synching problem.		
	Does TrAPSS have text processing capability that links annotations to disease information?		
	- No, but we have been thinking about this.		
	Does the primer-picking tool only select primers from exons? (Yajun Yi)		
	- The tool used is Primer 3 and can it can be used design primers to introns or		

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exons. The C version has been implemented, incorporated with a Java wrapper.

Is BLAST analysis part of the primer picking algorithm? (Yajun Yi)

- No. We don't have enough resource to Blast primers against whole genome. Primer selection process relies on expert users.

Genomic coordinates are often not accurate. Add to this the complication of multiple splice variants. The Golden Path assembly is considered better than Ensembl. (Yajun Yi)

- We currently use Ensembl. We use the archival approach and document different versions of genes.

Does TrAPSS have security feature that allows different levels of access to the data? (Juli Klemm)

- Yes, we have implemented the UNIX model of security.

Is there any plan to add a subject dimension, a subject-centric view? (Mark Watson)

- This is a very interesting point. We are currently focused on annotation, but this is a great idea.

# Other Items Discussed

- Please send Juli any feedback on the agenda of the face-to-face meeting. Also let Juli know who from your center is attending the meeting.
- Next meeting falls on Labor Day, and will be re-scheduled.

#### **Action Items:**

Name Responsible	Action Item	Date Due	Notes	
Juli Klemm	Distribute meeting minutes	8/9/04		
Juli Klemm	Re-schedule for the next meeting	8/9/04		